1/8

JUL 19 2002 80

09.07.02

RECEIVED

JUL 2 9 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Forschungszehtrum Juelich GmbH

<120> Process for the microbial production of amino acids by boosted activity of export carriers

<130> 1

<140> PCT/DE96/02485

<141> 1996-12-18

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1016)..(1726)

<400> 1

ccatttgctg aaggtgttac tctgcctggc caattcctg cgggcgaaga agtgaaaaac 60

cctgaacctt ttcagaagta actaaggccg catccctcg attgctgcat caacgacggc 120

gtctgtgagt ctagctagag atctagattc capgcgccat cgttgccaat acatcggtgt 180

gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240

ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300

cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360

acggtcttga agcacatctt tgggaccgaa gcgtaa gacg ggcatcgcag cccaatctag 420

tttcccatca accatgtagg catcccgcaa tgagggggtt gcaatggcca agtggcgcat 480

ggttccaagt tetactaett cacateeege cacgggatta gettcaeggg ttacegetee 540

taaaacatet eeacgeegea geaaggataa tgtgtgeget teatetteea agegeagegt 600

gagcgttgct ccaccccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660

cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttgcgc 720

tttagtttct gcttgcagca acaccatttt ccgcgctgct tgcacaagga cttcacccgc 780

ttcggttgct ttggccggtt gggtgcgcga taccaacact cgacccacgt gatgctcgag 840

agctttaacg cgctgactca ccgccgaggg ggaaatggaa aggtgctaagg aggcgccttc 900

gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaadggggt tcatgaagct 960

atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018
Met

1

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Gly Ala Ser Leu 5 10 15	1066					
tta ctg tcc atc gga ccg cag att gta ctg gtg att aaa caa gga att Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile 20 25 30	1114					
aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac Lys Arg Glu Gly Leu Ile Ala Val 35 40 45	1162					
gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn 50 55 60 65	1210					
gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr 70 75 80	1258					
ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys 85 90	1306					
gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp 100 105 110	1354					
gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg 115 120 125	1402					
gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro 130 135 140 145	1450					
atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg Met Leu Met Ala Ile Val Leu Thr Trp Leu Ash Pro Asn Ala Tyr Leu 150 155 160	1498					
gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr 165 170 175	1546					
gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gda agc ctg atc tgg Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp 180 185	1594					
ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser 195 200 205	1642					
age ece aag gtg tgg ege tgg ate aac gte gte gtg gea gtt gtg atg Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met 210 215 220 225	1690					
acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly 230 235	1736					
ttttggaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtgggaa atctcatcga 1						
tcgcctccaa ctcggcgtca gaaaactcca agttgttgag tgaatcaagg						

getgeteace tgacgaagea ceaateaatg cactggteac ggtateegeg cegtaetete 1916
ettgetegeg cagcaeceat geaagegeea tetgegeaag tgactgeeg egtteetggg 1976
egatgteatt gagettgegg accatateaa tattgtteac gtteaacatg eceteagaea 2036
gggaettace etggetggeg egggaageet etggaattee ategagatat ttgteegtga 2096
geaggeeetg egeaagtggt gagaaageaa tgacgeeaag accattgttg geagetgaet 2156
geaacaagtt eteaeegtea tegeeeggtt eeteegeeaa aegattaatg atggaatage 2216
ttggetgatg aateagaage gggeageeet eeteegeeat gaacteagee geeteegetg 2276
tgagetetgg accgtaggaa gaaataecea egtaaagage ettteeagae geaacaatgt 2336
caegeaatge gtacatggtt tetteeaaag gagtatet 2374

<210> 2
<211> 236
<212> PRT (LysE)
<213> Corynebacterium glutamicum

<400> 2

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Gly Ala Ser

1 5

Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Val Cys Leu Ile Ser
35 40 45

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser 50 55 60

Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala 65 70 75 80

Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro 100 105 110

Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn 115 120 125

Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
130 135 140

Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Ash Pro Asn Ala Tyr 145 150 155 160

Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile 180 185 190

```
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
                             200
Ser Ser Pro Lys Val Trp Arg Tip Ile Asn Val Val Ala Val Val
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
                     230
<210> 3
<211> 2374
<212> DNA (complement to <210>
<213> Corynebacterium glutamicum
<221>unsure
<222>CDS (2)..(652)
<223>orf3
<220>
<221>gene
<222>CDS (1421)..(2293)
<223>LysG
<400> 3
a gat act eet ttg gaa gaa ace atg tåe gea ttg egt gae att gtt geg 49
  Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
tet gga aag get ett tae gtg ggt att tet tee tae ggt eea gag ete
                                                                      97
Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg
Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
att cat cag cca age tat tee ate att aat 
otinggt tgg gtg gag gaa eeg
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
gge gat gae ggt gag aac ttg ttg cag tea gdt gee aac aat ggt ett
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
ggc gtc att gct ttc tca cca ctt gcg cag ggc√ctg ctc acg gac aaa
                                                                      289
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly\Leu Leu Thr Asp Lys
tat etc gat gga att eea gag ggt tee ege gee a\ge eag ggt aag tee
                                                                      337
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
ctg tct gag ggc atg ttg aac gtg aac aat att gat\atg gtc cgc aag
                                                                      385
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
        115
                             120
ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt dcg cag atg gcg
                                                                      433
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu A↓a Gln Met Ala
    130
                         135
                                              140
```

ctt gca·tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val 145 150 160	481
acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser 165 170 175	529
ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg Leu Asp Ser Leu Asn Asn Leu Glu Phe 180 185 185 190	577
atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala 195 200 205	625
acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat Thr Asp Ser Lys Thr Arg Glu Asn 210 215	672
ggccaatgcg gtcatcacaa ctgccacgac gacgttgatc cagcgccaca ccttggggct	732
ggacagcggg cgtgacaatg ctgctgcgcc gaaadccacc agcgggaacc agatcaggct	792
tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac	852
gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat	912
tgccatcaac atgggcttta cccaaacccg ctgcttatcg acgctcacct ccacccgcac	972
ccggttgcgc gtgtcagtgg ccaccgccga accgccqaaa ggcgtgtcat cgggcacggt	1032
tggttctgtt tcttcaatga tctgtggcgc ttccaccettg tttgtcatgg cgtctttcgc	1092
tgccatgacg gcaaaccata acaggtaage gatgccacc cagcgcataa tatcgagcac	1152
gatcggcgcg gcattggaca aaagatcaac gcccaaggtg ccggcgatga acaaaaagac	1212
gtcagaaatt aaacacacga gaagaaccgc aatgagtcqt tcgcgcttaa ttccttgttt	1272
aatcaccagt acattetgeg gteegatgga cagtaaaaga etggeeecca aaagcagace	1332
tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt	1392
ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act Met Asn Pro Ile Gln Leu Asp Thr 220 225	1444
ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala 230 235 240	1492
ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu 245 250 255	1540
cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala 260 265	1588
acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu	1636

275	280	e	285				
			cġc ctt gct gaa Arg Leu Ala Glu				
			tcc aca tgg ttt Ser Thr Trp Phe 320				
	n Glu Va\l Ala		gca acg ctc acg Ala Thr Leu Thr 335				
			ctg cgg cgt gga Leu Arg Arg Gly 350				
		du Ala Asn Pro	gtg gcg gga tgt Val Ala Gly Cys 365				
			att gca acc ccc Ile Ala Thr Pro				
			gat tgg gct gcg Asp Trp Ala Ala 400				
ccc gtc tta cg Pro Val Leu Ar 40	g Phe Gly Pro	aaa gat gtg ctt Lys Asp Val Leu 410	caa gac cgt gac Gln Asp Arg Asp 415	ctg 2020 Leu			
			cgc gta tcc att Arg Val Ser Ile 430				
		Glu Ala Ile Arg	cga ggc ctt ggt Arg Gly Leu Gly 445				
			cta aaa gca gga Leu Lys Ala Gly				
			ccg atg tat tgg Pro Met Tyr Trp 480				
	u Glu Ser Arg		ctc aca gac gcc Leu Thr Asp Ala 495				
gtt gat gca gc Val Asp Ala Al 500			ttacttctda aaagg	ttcag 2313			
ggtttttcac ttcttcgccc gcaggaattg ggccaggcag agtaacacct tcagcaaatg 2373							
g			\	2374			

35

```
<210> 4
<211> 216
<212> PRT (orf3)
<213> Corynebacterium \glutamicum
<400> 4
Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
Ile His Gln Pro Ser Tyr Ser 1\text{le Ile Asn Arg Trp Val Glu Glu Pro
Gly Asp Asp Gly Glu Asn Leu Le\psi Gln Ser Ala Ala Asn Asn Gly Leu
                     70
Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
Tyr Leu Asp Gly Ile Pro Glu Gly Set Arg Ala Ser Gln Gly Lys Ser
            100
                                 105
                                                      110
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
                             120
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gl\n Ser Leu Ala Gln Met Ala
    130
                        135
                                             140
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
                    150
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
                                     170
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
                                 185
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
                                                 205
Thr Asp Ser Lys Thr Arg Glu Asn
    210
<210> 5
<211> 290
<212> PRT (LysG)
<213> Corynebacterium glutamicum
<400> 5
Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
                                      10
Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu 🕻 al
```

40

Ser Arg. Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu The Pro Leu Thr Ile Ala Ile Asn Ala 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Val Phe Asn Glu Val Ala Ser

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr

115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
165 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
195 200 205

Gly Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala 225 230 239 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu 275 280 285

Arg Pro 290

FZJ 9910 PCT/US 6/8

FZJ 9910 PCT/US 8/8